

phantom, using their clinical method and prescription dose. EBT3 GafChromic film was used to measure an axial plane of dose. Pins in the phantom facilitated alignment of the film and calculated dose planes. Gantry linac and Cyberknife centres were audited, using a variety of TPS with pencil beam, AAA, CCC, Acuros and Monte Carlo algorithms. Scanned films were compared to dose distributions calculated by the individual centres, using single red-channel dosimetry and a purpose-built Matlab application. Centres were also asked to irradiate additional calibration films to provide output-normalised optical density to dose calibration. Measured and calculated isodoses corresponding to 120, 100, 70 and 50% of prescription dose were compared (figure 1), and conformity and maximum distance to agreement were measured. For the areas bound by the 100, 50 and 30% calculated isodoses, local gamma analysis, mean gamma and gamma pass rate (at 3%, 2mm) and a mean dose comparison was performed. The latter was compared to the alanine dosimetry results.

**Results:** The dosimetry of the calibration films was reproducible to  $\pm 0.9\%$  (1.S.D), for doses ranging from 4.3 to 26.9 Gy.

The audit relative dosimetry results are reported in table 1. Mean dose differences within the 100% calculated isodose line agreed well with alanine dosimetry;  $-0.1 \pm 2.0\%$  (1.S.D). Gamma pass rates (%) and mean gamma results varied with some outlying measurements, mostly caused by small dose deviations within the PTV or at low doses. Isodose line agreement (figure 1) was generally much closer at the 70 and 100% dose levels, indicated by the lower S.D. (table 1, column 5). The exception was the centre using a pencil beam algorithm, where the measured prescription dose covered a significantly smaller area than that calculated, consistent with the algorithm's known limitations calculating dose in low density lung surrounding tumour.

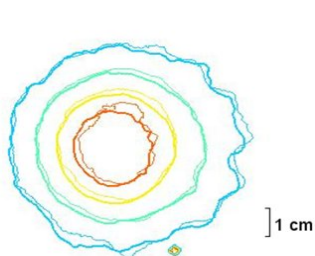


Figure 1. Agreement between measured (thin line) and calculated (bold line) 50, 70, 100 and 120% prescription isodose lines. Crosses correspond to phantom pins.

% of prescription dose*	Within the calculated isodose line*			Maximum distance between measured and calculated isodose lines: audit mean (mm) $\pm 1$ S.D
	Mean dose difference: % $\pm 1$ S.D	% of measurements achieving Gamma pass rates in the ranges: 0-50, 50-75, 75-100	% of measurements achieving mean Gamma in the ranges: <1, 1-2, >2	
120	-	-	-	0.5 $\pm$ 5.2
100	0.30 $\pm$ 2.65	22, 22, 57	70, 22, 9	1.1 $\pm$ 3.5
70	-	-	-	1.2 $\pm$ 3.4
50	-0.24 $\pm$ 2.87	0, 26, 74	83, 17, 0	3.4 $\pm$ 5.8
30	-0.85 $\pm$ 2.84	9, 48, 43	70, 26, 4	-

Table 1. Collated relative dosimetry audit results.

**Conclusions:** Of the 21 UK centres audited, 74% of measurements were within  $\pm 3\%$  agreement compared to calculated doses. Where appropriate, outlying centres have been offered support from the QA Group to bring their results into line.

The EBT3 GafChromic film was found to be highly suited to a postal audit, reliably giving detailed information about the geometric and dosimetric accuracy of treatment.

#### OC-0155

##### UK SABR Consortium Lung Dosimetry Audit; absolute dosimetry results

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**Purpose/Objective:** The UK SABR Lung Consortium dose audit was designed to assess the positional and dosimetric accuracy of SABR lung treatment delivery. The audit has been carried out in 21 radiotherapy centres between October 2013 and July 2014 in order to provide an independent check of safe implementation and to identify problems in the modelling and delivery of SABR lung treatment.

**Materials and Methods:** A mail based audit using EBT3 GafChromic film and alanine dosimeters was designed. A CIRS Model 002LFC anthropomorphic thorax phantom which contained 9 adjacent alanine pellets in the tip of a Farmer chamber shaped insert was scanned, structure sets for the ITV and alanine pellets were pre-delineated, and was sent to radiotherapy centres to be loaded into their treatment planning system. Each centre used this CT scan set to create a SABR plan using their current planning protocol (including dose, fractionation and coverage) and technique. The centres used their own margin to create the PTV. A range of delivery techniques were used including conformal, VMAT and Cyberknife and calculated using local algorithms (AAA, Collapsed Cone, Monte Carlo and Pencil beam). The doses determined by the alanine dosimeters were compared to expected doses determined by treatment plan system (TPS) calculation, film and local ionisation chamber measurements.

**Results:** The mean % difference between the alanine measured doses, the TPS calculated doses, and the local chamber measurements found to be within 2% (1 SD) as given in table 1. As shown, alanine findings were supported by the film results.

Table 1: The mean percentage difference between the alanine results with TPS, farmer chamber and film stated with one standard deviation (k=1).

Dosimetry systems	Mean % differences $\pm 1$ S.D
Alanine and TPS	0.2 (+/- 2.0)
Alanine and local farmer chambers	-0.4 (+/- 1.8)
Alanine and film	-0.1 (+/- 2.0)

There was no significant difference between the performance of AAA and Monte Carlo algorithms (mean difference of 0.2% (+/- 1.3) versus 0.4% (+/- 2.1)), while a mean difference of 1.4% (+/- 1.0) was seen when the collapsed cone algorithms were used. The pencil beam algorithm significantly overestimated the dose (-5.04%).

Across all algorithms, the mean differences in regards to delivery techniques varied by 0.6% (+/- 1) and -0.1% (+/- 1.5) using Conformal and VMAT respectively. The results for the Cyberknife delivery technique were at either end of distribution curve, with the pencil beam overestimating the dose and the Monte Carlo algorithm making a slight underestimation (figure 1).

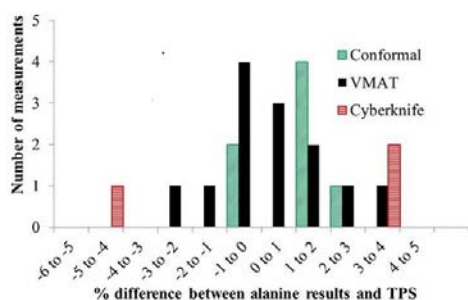


Figure 1: Percentage difference between alanine measurement and TPS by delivery technique.

**Conclusions:** A dosimetric audit has been successfully carried out of Lung SABR implementation in 21 radiotherapy departments of UK. The absolute dosimetry results show that modelling and delivery of Lung SABR was within 3% accuracy for 18/21 (or 86%) of centres, suggesting that the implementation of Lung SABR has been carried out accurately.

**Proffered Papers: Physics 4: Protons and light ions from nano to macro**

#### OC-0156

##### Calculation of electron track structure in water and DNA medium

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**Purpose/Objective:** A challenge in ion-beam therapy is the inaccurate quantification of the biological effectiveness due to the assumption that the biological dose response to ions is comparable to high-energy photon beams. This is due to the high LET of the ions and their secondary electrons, leading to a high amount of energy deposition within a few nanometers. These energy depositions form a pattern, i.e. a particle track structure, which is strongly correlated to the DNA damage. This pattern can be characterised by nanodosimetric quantities, calculated by Monte Carlo simulations.

Track structure simulations require the implementation of cross section data for the interaction of the incident particles and their secondaries with molecules of the medium. Biological matter is conventionally represented by liquid water, as cross section data of DNA constituents have not yet been available.

The objective of this work was to facilitate improved electron track structure simulations by an evaluated cross section set of DNA constituents.

**Materials and Methods:** Models for electron-impact cross sections of the DNA constituents tetrahydrofuran, trimethylphosphate, pyrimidine and purine were developed on the basis of measured absolute differential and total scattering cross sections. The evaluated cross section data set was implemented in the Monte Carlo code PTrA to simulate electron track structure in DNA medium. Nanodosimetric quantities were calculated by track structure simulations of electrons with energies below 1 keV in water and DNA medium. The differences in simulation results obtained in the different media were analysed.

**Results:** It was found that the cross sections for water and DNA constituents show significantly different angular and energy dependences (for example, total ionisation cross

sections of DNA constituents are as much as a factor of two higher than those of water). Consequently, the simulated electron track structure in water and DNA medium indicates a significant underestimation of the initial DNA damage when using water cross sections.

**Conclusions:** An experiment-based cross section data set for interactions of secondary electrons of energies between 9 eV and 1 keV with DNA constituents was developed for use in track structure simulations. The simulated electron track structure in DNA medium reveals an underestimation of DNA damage when calculated using water cross sections.

#### OC-0157

##### Initial DNA damage patterns with Monte Carlo tracks and ionization clusters

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**Purpose/Objective:** The BioQuaRT group (Palmans et al., *BRJ* 2014) has recognized that experimental measurements of ionization clusters using nanodosimeters and Monte Carlo (MC) track structure simulations can be used to standardize the characterization of proton and light ion beam radiation quality and biological effectiveness. In this work, initial radiation damage patterns (i.e. DNA strand breaks from direct radiation effects) are obtained for proton, Li ion, and Co-60 beams, using two distinct methods: track superposition on top of a geometrical DNA model and cluster analysis using a probabilistic DNA model.

**Materials and Methods:** The MC code LlonTrack (Bäckström et al., *Med.Phys.*, 40, (6)) was used for the event-by-event track simulation (transport cutoff of 50 eV) of proton, lithium ion and Co-60 beams, which were then superimposed on top of a geometrical nucleosome model composed of 198 base pairs (bps). A strand break was scored when at least one ionization was located in a sugar-phosphate group, modeled as a cylindrical shell sector with volume equal to 0.13 nm<sup>3</sup>. The yields of single strand break (ssb) and double strand break (dsb) clusters were obtained for single-track and 2 Gy fractions to study inter-track effects. The generated tracks were also grouped into clusters using DBSCAN, a density based clustering algorithm (Ester et. al. 1996), and subsequently convolved with a probabilistic DNA model, to obtain ssb and dsb cluster yields for the single-track method. This novel probabilistic DNA model gives the probability of creating opposite strand damage within 10 bps as a function of the distance ( $p_{os}(d_{ij})$ ) between two ionizations  $i$  and  $j$  (see Figure). The probability of a cluster being a no-strand-break (nsb), an ssb, or a dsb cluster are given by

$$P_{nsb} = (1 - p)^n;$$

$$P_{dsb} = 1 - \prod_{j=1}^n [1 - p(1 - \prod_{i=1}^n [1 - p_{os}(d_{ij})])];$$

$$P_{ssb} = 1 - P_{nsb} - P_{dsb},$$

where  $n$  is the number of ionizations in the cluster and  $p$  is the site-hit probability.